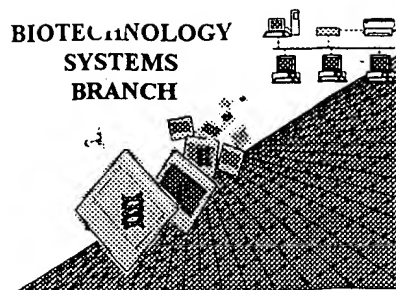


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/936,883

Source: PUT/09

Date Processed by STIC: 10/4/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

**<http://www.uspto.gov/web/offices/pac/checker>**

PCT09

## RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/936,883

TIME: 10:11:25

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

Does Not Comply  
Corrected Diskette Needed

pp 1-4

OK

4 <110> APPLICANT: Miyata, Toshio  
 6 <120> TITLE OF INVENTION: A METHOD FOR DETECTING MEGSIN PROTEIN  
 7 AND USE THEREOF  
 9 <130> FILE REFERENCE: SHIM012  
 11 <140> CURRENT APPLICATION NUMBER: US/09/936,883  
 12 <141> CURRENT FILING DATE: 2001-09-07  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01646  
 15 <151> PRIOR FILING DATE: 2000-03-17  
 17 <150> PRIOR APPLICATION NUMBER: 11/75305  
 18 <151> PRIOR FILING DATE: 1999-03-19  
 20 <150> PRIOR APPLICATION NUMBER: 11/306623  
 21 <151> PRIOR FILING DATE: 1999-10-28  
 23 <160> NUMBER OF SEQ ID NOS: 21  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1867  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Homo sapiens  
 32 <400> SEQUENCE: 1  
 33 atggcctccc ttgctgcagc aaatgcagag ttttgcctca acctgttcmr aasruaaaaa 60  
 E--> 34 aasnaaguhc yshasuhag agagatggat gacaatcaag gaaatggaaa tgtgttcttt 120  
 E--> 35 tctcttargg umtasasasn gngyasngya snvahhsrsr ctgagcctct tegetgacct 180  
 E--> 36 ggccctgggc cgcttgggag ctcaagatus ruhaaaauaa uvaargugya agnasgactc 240  
 E--> 37 cctctctcag attgataagt tgcttcatgt taacactgcc tcaassrusr gnasyuuhs 300  
 E--> 38 vaasnthraa srggatatgg aaactcttct aatagtcagt cagggctcca gtctcaactg 360  
 E--> 39 gytyrgyasn srsrasnsrg nsrgyugnsr gnuaaaagag ttttttctga tataaatgca 420  
 E--> 40 tcccacaagg attatgatct cysargvahs rasasnaasr hsystasyra suagcattgt 480  
 E--> 41 gaatgggctt tttgctgaaa aagtgtatgg ctttcataag srvaasngyu haaguysvat 540  
 42 yrgyhhsysg actacattga gtgtgccgaa aaattatacg atgccaaagt ggagcgaast 600  
 43 yrgucysaag uysutyrasa aysvaguarg qttgacttta cgaatcattt agaagacact 660  
 E--> 44 agacgtaata ttaataagva ashtthrasnh suguasthra rgargasnas nystggggtg 720  
 E--> 45 aaaatgaaac acatggcaca atcaagaacg tgattgggtga atrvaguasn guthrhsgyy 780  
 E--> 46 sysasnvygy guggtgagcat aagctcatct gctgtaattg tgctgggtgaa tgctgtgtac 840  
 E--> 47 ggyysrsrsr aavamtvaav aasnaavaty rttcaaaggc aagtggcaat cagccttcac 900  
 E--> 48 caagagcgaa accataaath ysgyystrgn sraahthrys srguthrasn tgccatttca 960  
 49 aatctcccaa gtgctctggg aaggcagtcg ccatgatgcy shshyssrry scyssrgyys 1020  
 50 aavaaamtmt catcaggaac ggaagtcca tttgtctgtt attgaggacc catcaatghs 1080  
 E--> 51 gnguarqysh asnsrvagu asrsrmtaag attcttgagc tcagatacaa tgggtggcata 1140  
 E--> 52 aacatgtacg ttctgysugu uargtyrasn gygyasnmmt yrvauctgcc tgagaatgac 1200  
 E--> 53 ctctctgaaa ttgaaaacaa actgaccttt cagurguasn asusrgugua snysuthrhg 1260  
 E--> 54 naatctaatt gaattggacca atccaaggcg aatgacctct aagtatgtta snumtguatr 1320  
 E--> 55 hrasnrarga rgmtthrsry styrvagagg tattttttcc tcagttcaag atagagaaga 1380  
 E--> 56 attatgaaat gaaaguvahh rgnhyguyas asntyrgumt yscaatattt gagagcccta 1440

see  
 item 9  
 on  
 Error  
 Summary  
 Sheet

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001

TIME: 10:11:25

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

E--> 57 gggctgaaag atattcttga tgaatccaaa gntyrurgaa augyuysash asgusrysgc 1500  
 58 agatctctct gggattgctt cggggggtcg tctgtatata tcaaggaaas usrgyaasrg 1560  
 59 ygyargutyr srargatgat gcacaaatct tacatagagg tcaactgagga gggcaccgag 1620  
 60 gctmtmthsy ssrtyrquva thrqugugyt hrguaaactg ctgccacagg aagtaatat 1680  
 E--> 61 gtagaaaagc aactccctca gtccthraaa athrgysras nvaguysgnu rgnsracgct 1740  
 62 gtttagagct gaccacccat tctattttgt tatcaggaag gatthruhar gaaashsrhu 1800  
 63 hvaargysas gacatcatct tattcagtgg caaagtttct tgcccttgaa suhsrgyyysv 1860  
 64 asrcysr 1867

item 9

item 9

313 <210> SEQ ID NO: 18  
 314 <211> LENGTH: 1938  
 315 <212> TYPE: RNA  
 316 <213> ORGANISM: Rattus norvegicus  
 318 <400> SEQUENCE: 18

"ts" not allowed in an  
RNA  
sequence

E--> 319 tttcaaaatg gcctcccttg ctgcagcaaa tgcagaattt ggcttcgacm taasruaaaa 60  
 E--> 320 aaasnaaguh gyhasttatt cagagagatg gatagtagtc aaggaaacgg aaatgtattc 120  
 E--> 321 ttcunarggu mtassrsrgn gyasngyasn vahhtcttcc ctgagcatct tcaactgcct 180  
 E--> 322 gagcctaate cgtttggttg ctsrsrusrh thraausrua rgugyaacga ggtgactgtg 240  
 E--> 323 nncgtcagat tgacaaggcc ctgcacttta tctccarggy ascysaaarg gnasyaauh 300  
 E--> 324 shsrccatca agacaaggga attcatcgaa cagtcagcta ggactgcaat atrsrarggn 360  
 E--> 325 gyasnsrsra snsrngugyu gntyrcaatt gaaagaggtt cttgctgaca taaactcatc 420  
 E--> 326 tcataaggat nnnngnuysar gvauaaasas nsrsrhsysa saaaaactca gcattgccaa 480  
 E--> 327 tggagttttt gcagagaaag tatttgattt tysusraas ngyvahaagu ysvahashca 540  
 E--> 328 taagagctat atggagtgtg ctgaaaactt atacaatgct aaagtghsys srtyrmtguc 600  
 E--> 329 ysaaguasnu tyrasnaays vagaaagagt tgattttaca aatgatatac aagaaaccag 660  
 E--> 330 atttaaaatt guargvaash thrasnasgn guthrarghy saataaatgg attgaaaatg 720  
 E--> 331 aaacacatgg caaaatcaag aagggtgttg snystrguas nguthrsgy ysysysvaug 780  
 E--> 332 gggacagcag cctcagctca tcagctgtca tgggtgctagt gaatgctgya ssrsrusrsr 840  
 E--> 333 sraavamtva uvaasnaagt ttacttcaaa ggcaagtgga aatcggcctt caccaagagt 900  
 E--> 334 gataccvaty rhysgyystr yssraahthr yssrasthrc tcagttgcca tttcaggtct 960  
 E--> 335 cccagcggtc ctggaaaaagc agttaatusr cyshshargs rrsrgyrgyy saavaasnat 1020  
 E--> 336 gatgcatcaa gaacggaggt tcaatttgtc taccattcag gagccamtmt hsgnguarga 1080  
 E--> 337 rghasnusrt hrgngurcca atgcagattc ttgagctaca atatcatggt ggcataagca 1140  
 E--> 338 tgtacrmtnu uguugntyrh sgygysrmtt yratcatggt gcccaggatgac tatctccg 1200  
 E--> 339 aaattgaaag caagctgagt mturguasas usrgugusry susrttcag aatctaattg 1260  
 E--> 340 actggacaaa tagcaggaag atgaaatctc aghgnasnum tatrthras nsrargysmt 1320  
 E--> 341 yssrgntatg tgaatgtgtt tctccccag ttcaagatag agaaagatta tgaatyrvaa 1380  
 E--> 342 snvahurgnh ysguysasty rguatgagga gccacttgaa atctgtaggc ttggaagaca 1440  
 E--> 343 tctttgttga gmtargsrhs uyssrvagyu guashvagut ccagggtgta tctgtctgga 1500  
 E--> 344 attgcctctg gaggtcgtct ctatgtasra rgaaasusrg yaasrgygya rgutyrvatc 1560  
 E--> 345 aaagctaatz cacaagtcce tcatagaggt ctgagaagaa ggcaccsrys umthsysru 1620  
 E--> 346 guvasrgugu gythrgagge aactgctgcc acagaaagta acatcgttga aaagctactt 1680  
 E--> 347 cctguaathr aaaathrgus rasnvaguys uurgaatcca cgggtgttcag agctgaccgc 1740  
 E--> 348 ccctttctgt ttgtcattag ggusrthrva hargaaasar gruhvaarg aagaatggca 1800  
 E--> 349 tcattctatt tactggcaaa gtctcgtgtc ctysasngyu hthrgyyysva srcysrtgaa 1860  
 E--> 350 attctatttg gttttccata cactaacagg catgaagaa catcataagt gaatagaatt 1920  
 E--> 351 gtaattggaa gtacatgg 1938

Per 1.823  
 of sequence

Rubs, a  
combined

DNA/RNA

sequence

requires

a <212>

response of

DNA; also,

Hyplain in

C2207-C2237  
 section that  
 sequence is a  
 combined  
DNA/RNA  
 10/4/01

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001

TIME: 10:11:25

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

```

356 <213> ORGANISM: Rattus norvegicus
358 <400> SEQUENCE: 19
359 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe
360 1 5 10 15
361 Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
362 20 25 30
363 Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly
364 35 40 45
E--> 365 Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser
366 50 55 60
367 Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu
368 65 70 75 80
E--> 369 Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu
370 85 90 95
371 Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys
372 100 105 110
373 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg
374 115 120 125
375 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys
376 130 135 140
377 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp
378 145 150 155 160
379 Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
380 165 170 175
381 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser
382 180 185 190
383 Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met
384 195 200 205
385 His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met
386 210 215 220
387 Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met
388 225 230 235 240
389 Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln
390 245 250 255
391 Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val
392 260 265 270
393 Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg
394 275 280 285
395 Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg
396 290 295 300
397 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys
398 305 310 315 320
399 Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala
400 325 330 335
401 Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser
402 340 345 350
403 Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn
404 355 360 365
405 Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

```

see item 9  
on Enon  
summary  
sheet

DATE: 10/04/2001

TIME: 10:11:25

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

```

406          375          380
409 <210> SEQ ID NO: 20
410 <211> LENGTH: 1848
411 <212> TYPE: DNA
412 <213> ORGANISM: Mus Musculus
414 <400> SEQUENCE: 20
415 ttcgacttat tcagagagat ggatagtagc caaggaaatg gaaatgtaha suharggumt 60
E--> 416 assrsrgrgy ashyashva ttcttctctt ccctgagcat cttcactgcc ctgaccctaa 120
417 tccgtctghh srsrusrhh raauthruar guggtgctcg aggtgactgt gcacgtcaga 180
E--> 418 ttgacaaggc actgcacttt gyaaarggya scysaaargg nasysaauhs haacatacca 240
E--> 419 tcaagacaag gaaactcatc taataatcag ccaggactta snrsrarggn gyasnsrsra 300
E--> 420 snasnrgry ucagtatcaa ttgaaaagag ttcttgctga cataaactca tctcataagg 360
E--> 421 ntyrgnuysa rgvauaaasa snsrshrshs gattatgaac tcagcattgc cactggagtt 420
422 tttgcagaaa aagtctatas tyrguusraa thrgyvahaa guysvatyrg actttcataa 480
E--> 423 gaactacatt gagtgtgctg aaaacttata caatgctash hsysasntyr gucysaagua 540
E--> 424 snutyrasna aaaagtggaa agagttgact tcacaaaatga tgtacaagat accagattty 600
E--> 425 svaguargva ashthrasna svagnasthr rghaaaatt aataaattga ttgaaaatga 660
E--> 426 gacacatgga aagatcaaga agysasnyst rguasnguth rhsgyysysy sgtgttgggc 720
427 gacagcagcc tcagctcgtc ggctgtcatg gtgctgggtg augyassrsr usrsrsraav 780
E--> 428 amtvaauvaa cgctgtttac ttcaaaggca aatggaaatc ggccttcacc aagactasna 840
429 avatyrrhysg yystryssra ahthrysthr gataccctca gttgccgttt taggtctccc 900
430 acgtgtcctg gaaaagtaas thrusrcysa rghargsrtr hrcysrgyys vagttaatat 960
E--> 431 gatgcatcaa gaacgggggt tcaatttgtc taccattcag vaasnmtmth sgnguargar 1020
E--> 432 ghasnusrth rgncagccac caatgcaggt tcttgagctc caatatcatg gtggcataag 1080
E--> 433 cgnrrmtgnv auguugntyr hsgygysrat gtacattatg ctgctgagg atggcctatg 1140
434 tgaatttqaa agcaagmtty rmturguasg yucysgugus rysctgagtt tcagaatct 1200
E--> 435 gatggactgg accaatagga ggaaaatgaa ausrhgnasn umtasttrthr asnargargy 1260
E--> 436 smtystctca gtatgtgaac gtgtttctcc cccagttcaa gatagagaag aatsrgntyr 1320
E--> 437 vaasnvhur gnhyshguysa sntatgaaat gacgcaccac ttgaaatcct taggcttgaa 1380
438 agatatcttt tyrgumtthr hshsuyssru gyuysashga tgagtcacgt gcagatctct 1440
439 ctggaattgc ctctggaggt cgtctcasgu srsraaasus rgyaasrgyg yargutacgt 1500
440 atcaaagcta atgcacaagt cattcataga ggtctcagag gagtyrvasr ysumthsyss 1560
441 rhquvasrgu guggcactga agccactgct gccacagaaa ataacattgt tgaaaagcag 1620
E--> 442 gythrguaat hraaaathrg uasnasnvag uysgmottee tgagtcaca gtgttcagag 1680
443 ccgaccgccc ctttctgttt gtcuurqsrt hrvtahgaa asarghuhv aatcaagaag 1740
E--> 444 aatgacatea tcttatttacc tggcacaagtc tcttgctcty sysasnasuh thrgyysvas 1800
445 rcysrtqaaa ttcgatttgg tttcttatac aqtaacagqc atcaagaa 1848

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001

TIME: 10:11:26

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:34 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1  
 M:340 Repeated in SeqNo=1  
 L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
 L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:137 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
 L:144 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
 L:144 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
 L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:156 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:156 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:161 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
 L:218 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
 L:319 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:15  
 L:320 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18  
 L:320 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
 L:320 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:27  
 M:340 Repeated in SeqNo=18  
 L:321 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
 L:321 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:39  
 L:322 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:322 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:50  
 L:323 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 L:323 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:59  
 L:324 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 L:324 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:68  
 L:325 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:325 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:79  
 L:326 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
 L:326 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:85  
 L:327 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14  
 L:327 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:99  
 L:328 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15  
 L:328 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:114  
 L:329 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
 L:329 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:124  
 L:330 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
 L:330 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:136  
 L:331 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
 L:331 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:143  
 L:332 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:332 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:154  
 L:333 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:333 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:165  
 L:334 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001

TIME: 10:11:26

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10042001\I936883.raw

L:334 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:178  
L:335 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
L:335 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:184  
L:336 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13  
L:336 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:197  
L:337 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:337 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:209  
L:338 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13  
L:338 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:222  
L:339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
L:339 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:232  
L:340 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
L:340 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:241  
L:341 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16  
L:341 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:257  
L:342 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
L:342 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:266  
L:343 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13  
L:343 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:279  
L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:344 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:291  
L:345 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:345 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:299  
L:346 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
L:346 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:309  
L:347 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:347 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:317  
L:348 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:348 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:329  
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15  
L:349 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:344  
L:350 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19  
L:350 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:363  
L:351 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5  
L:351 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:368  
L:365 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19  
M:340 Repeated in SeqNo=19  
L:416 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
M:340 Repeated in SeqNo=20

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/936,883

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    "(NEW RULES)"  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.